

## RAW SEQUENCE LISTING

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Application Serial Number: 19/805,075

Source: IFW

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IFWO

## RAW SEQUENCE LISTING

DATE: 01/13/2005

PATENT APPLICATION: US/10/805,075

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3 <110> APPLICANT: Johnson, Jeffrey D.
4     Gregoire, Francine M.
5     Schweitzer, Anthony
6     Terasawa, Yuko
7     Wilson, Maria S.
8     Blume, John E.
9     Metabolex, Inc.
11 <120> TITLE OF INVENTION: Compositions and Methods of Using Hexokinase V
13 <130> FILE REFERENCE: 016325-008110US
15 <140> CURRENT APPLICATION NUMBER: US 10/805,075
16 <141> CURRENT FILING DATE: 2004-03-19
18 <150> PRIOR APPLICATION NUMBER: US 60/456,650
19 <151> PRIOR FILING DATE: 2003-03-20
21 <160> NUMBER OF SEQ ID NOS: 26
23 <170> SOFTWARE: PatentIn Ver. 2.1
25 <210> SEQ ID NO: 1
26 <211> LENGTH: 2754
27 <212> TYPE: DNA
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82 &lt;210&gt; SEQ ID NO: 2

83 &lt;211&gt; LENGTH: 917

84 &lt;212&gt; TYPE: PRT

85 &lt;213&gt; ORGANISM: Homo sapiens

87 &lt;220&gt; FEATURE:

88 &lt;223&gt; OTHER INFORMATION: human hexokinase V (HKV, HK5)

90 &lt;400&gt; SEQUENCE: 2

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95             20             25             30
97 Asp Asp Thr Leu Leu Asp Ile Met Arg Arg Phe Arg Ala Glu Met Glu
98             35             40             45
100 Lys Gly Leu Ala Lys Asp Thr Asn Pro Thr Ala Ala Val Lys Met Leu
101             50             55             60
103 Pro Thr Phe Val Arg Ala Ile Pro Asp Gly Ser Glu Asn Gly Glu Phe
104             65             70             75             80
106 Leu Ser Leu Asp Leu Gly Gly Ser Lys Phe Arg Val Leu Lys Val Gln
107             85             90             95
109 Val Ala Glu Glu Gly Lys Arg His Val Gln Met Glu Ser Gln Phe Tyr
110             100            105            110
112 Pro Thr Pro Asn Glu Ile Ile Arg Gly Asn Gly Ile Glu Leu Phe Glu
113             115            120            125
115 Tyr Val Ala Asp Cys Leu Ala Asp Phe Met Lys Thr Lys Asp Leu Lys

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119 145      150      155      160
121 Thr Lys Leu Glu Glu Gly Val Leu Leu Ser Trp Thr Lys Lys Phe Lys
122      165      170      175
124 Ala Arg Gly Val Gln Asp Thr Asp Val Val Ser Arg Leu Thr Lys Ala
125      180      185      190
127 Met Arg Arg His Lys Asp Met Asp Val Asp Ile Leu Ala Leu Val Asn
128      195      200      205
130 Asp Thr Val Gly Thr Met Met Thr Cys Ala Tyr Asp Asp Pro Tyr Cys
131      210      215      220
133 Glu Val Gly Val Ile Ile Gly Thr Gly Thr Asn Ala Cys Tyr Met Glu
134 225      230      235      240
136 Asp Met Ser Asn Ile Asp Leu Val Glu Gly Asp Glu Gly Arg Met Cys
137      245      250      255
139 Ile Asn Thr Glu Trp Gly Ala Phe Gly Asp Asp Gly Ala Leu Glu Asp
140      260      265      270
142 Ile Arg Thr Glu Phe Asp Arg Glu Leu Asp Leu Gly Ser Leu Asn Pro
143      275      280      285
145 Gly Lys Gln Leu Phe Glu Lys Met Ile Ser Gly Leu Tyr Leu Gly Glu
146      290      295      300
148 Leu Val Arg Leu Ile Leu Leu Lys Met Ala Lys Ala Gly Leu Leu Phe
149 305      310      315      320
151 Gly Gly Glu Lys Ser Ser Ala Leu His Thr Lys Gly Lys Ile Glu Thr
152      325      330      335
154 Arg His Val Ala Ala Met Glu Lys Tyr Lys Glu Gly Leu Ala Asn Thr
155      340      345      350
157 Arg Glu Ile Leu Val Asp Leu Gly Leu Glu Pro Ser Glu Ala Asp Cys
158      355      360      365
160 Ile Ala Val Gln His Val Cys Thr Ile Val Ser Phe Arg Ser Ala Asn
161      370      375      380
163 Leu Cys Ala Ala Ala Leu Ala Ala Ile Leu Thr Arg Leu Arg Glu Asn
164 385      390      395      400
166 Lys Lys Val Glu Arg Leu Arg Thr Thr Val Gly Met Asp Gly Thr Leu
167      405      410      415
169 Tyr Lys Ile His Pro Gln Tyr Pro Lys Arg Leu His Lys Val Val Arg
170      420      425      430
172 Lys Leu Val Pro Ser Cys Asp Val Arg Phe Leu Leu Ser Glu Ser Gly
173      435      440      445
175 Ser Thr Lys Gly Ala Ala Met Val Thr Ala Val Ala Ser Arg Val Gln
176      450      455      460
178 Ala Gln Arg Lys Gln Ile Asp Arg Val Leu Ala Leu Phe Gln Leu Thr
179 465      470      475      480
181 Arg Glu Gln Leu Val Asp Val Gln Ala Lys Met Arg Ala Glu Leu Glu
182      485      490      495
184 Tyr Gly Leu Lys Lys Lys Ser His Gly Leu Ala Thr Val Arg Met Leu
185      500      505      510
187 Pro Thr Tyr Val Cys Gly Leu Pro Asp Gly Thr Glu Lys Gly Lys Phe
188      515      520      525

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190 Leu Ala Leu Asp Leu Gly Gly Thr Asn Phe Arg Val Leu Leu Val Lys
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193 Ile Arg Ser Gly Arg Arg Ser Val Arg Met Tyr Asn Lys Ile Phe Ala
194 545      550      555      560
196 Ile Pro Leu Glu Ile Met Gln Gly Thr Gly Glu Glu Leu Phe Asp His
197      565      570      575
199 Ile Val Gln Cys Ile Ala Asp Phe Leu Asp Tyr Met Gly Leu Lys Gly
200      580      585      590
202 Ala Ser Leu Pro Leu Gly Phe Thr Phe Ser Phe Pro Cys Arg Gln Met
203      595      600      605
205 Ser Ile Asp Lys Gly Thr Leu Ile Gly Trp Thr Lys Gly Phe Lys Ala
206      610      615      620
208 Thr Asp Cys Glu Gly Glu Asp Val Val Asp Met Leu Arg Glu Ala Ile
209 625      630      635      640
211 Lys Arg Arg Asn Glu Phe Asp Leu Asp Ile Val Ala Val Val Asn Asp
212      645      650      655
214 Thr Val Gly Thr Met Met Thr Cys Gly Tyr Glu Asp Pro Asn Cys Glu
215      660      665      670
217 Ile Gly Leu Ile Ala Gly Thr Gly Ser Asn Met Cys Tyr Met Glu Asp
218      675      680      685
220 Met Arg Asn Ile Glu Met Val Glu Gly Gly Glu Gly Lys Met Cys Ile
221      690      695      700
223 Asn Thr Glu Trp Gly Gly Phe Gly Asp Asn Gly Cys Ile Asp Asp Ile
224 705      710      715      720
226 Arg Thr Arg Tyr Asp Thr Glu Val Asp Glu Gly Ser Leu Asn Pro Gly
227      725      730      735
229 Lys Gln Arg Tyr Glu Lys Met Thr Ser Gly Met Tyr Leu Gly Glu Ile
230      740      745      750
232 Val Arg Gln Ile Leu Ile Asp Leu Thr Lys Gln Gly Leu Leu Phe Arg
233      755      760      765
235 Gly Gln Ile Ser Glu Arg Leu Arg Thr Arg Gly Ile Phe Glu Thr Lys
236      770      775      780
238 Phe Leu Ser Gln Ile Glu Ser Asp Arg Leu Ala Leu Leu Gln Val Arg
239 785      790      795      800
241 Arg Ile Leu Gln Gln Leu Gly Leu Asp Ser Thr Cys Glu Asp Ser Ile
242      805      810      815
244 Val Val Lys Glu Val Cys Gly Ala Val Ser Arg Arg Ala Ala Gln Leu
245      820      825      830
247 Cys Gly Ala Gly Leu Ala Ala Ile Val Glu Lys Arg Arg Glu Asp Gln
248      835      840      845
250 Gly Leu Glu His Leu Arg Ile Thr Val Gly Val Asp Gly Thr Leu Tyr
251      850      855      860
253 Lys Leu His Pro His Phe Ser Arg Ile Leu Gln Glu Thr Val Lys Glu
254 865      870      875      880
256 Leu Ala Pro Arg Cys Asp Val Thr Phe Met Leu Ser Glu Asp Gly Ser
257      885      890      895
259 Gly Lys Gly Ala Ala Leu Ile Thr Ala Val Ala Lys Arg Leu Gln Gln
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262 Ala Gln Lys Glu Asn

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267 <211> LENGTH: 3788
268 <212> TYPE: DNA
269 <213> ORGANISM: Homo sapiens
271 <220> FEATURE:
272 <223> OTHER INFORMATION: human hexokinase V variant
274 <400> SEQUENCE: 3
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**VERIFICATION SUMMARY**

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